Inheritance of Seeds Color and Some Economic Characters in Pea (*Pisum sativum* L.) El-Dakkak, A. A. A Horticulture Research Institute, Agricultural Research Center, Giza, Egypt



### ABSTRACT

The present study was carried out during four growing winter seasons (2012/2013 to 2015/2016) at Shandweel Agricultural Research Station, Research Center Ministry of Agriculture Egypt. The basic material used in this study consisted of (Master-B x Mammoth melting sugar) F<sub>1</sub> hybrid which all plants have purple flowers and both round and mottled in seed shape and color, respectively and planted to produce F<sub>2</sub> population which isolated two population categories (purple flowers, mottled seeds and white flowers, green seeds). Data of both F3 and F4 generations were studied in four groups, *i.e.* Wrinkled green seed, Round green seed, Round mottled seed and Wrinkled mottled seed. Analysis of variance showed significant differences among the genotypes for all characters. Mean values for F<sub>1</sub> generation were high in shilling %, no. of pods/plant and green pod yield. Estimates of the genetic parameters from the generation means indicated significant both additive [d] and dominance [h] gene effects in some traits of the base population, i.e. plant height, No. of pods/ plant, Shelling %, 100-fresh seed weight and Fresh pod yield/plant. Inbreeding depression in green seeds segregations was uniformly less in magnitude than that obtained in the mottled seeds segregations. Most  $F_2$  progenies showed strong evidence of transgressive segregation above the parental values of both green and mottled seed segregations in most traits. Small differences were observed between PCV and GCV for all the characters. High heritability associated with high genetic advance was observed for most studied characters. The potence ratio displayed over dominance in the inheritance of Pod length, Pod weight, No. of pods/ plant, Shelling% and fresh pod yield plant. The estimates of broad sense heritability after the end cycle of selection were medium for number of seeds/pod in the wrinkled (52.33%), round (50.65%) of green seed and only round of mottled seed (56.74%), while it was of high magnitude for each of all other traits in all categories. From the results, therefore, it is demonstrated that a considerable amount of readily fixable variation is present and available for the plant breeder to manipulate. It could be noticed that selection for plant height trait in mottled seed (Round and wrinkled) category and for pod green yield trait in only round seed category generally, was better than any other categories over all comparisons after the 2<sup>nd</sup> cycle. Means of 100-seeds weight, No. of pods/ plant and fresh pods yield were higher in round seed compared with wrinkled one of both green and mottled seed while No. of seeds/pod exhibited the reverse trend in both F<sub>3</sub> and F<sub>4</sub> generations.

## **INTRODUCTION**

Pea (Pisum sativum L.) is one of the important favorable vegetable crops grown in Egypt. To develop a new variety there is need of the magnitude of genetic variability in the base material and the vast of variability for desired characters. However, a good knowledge on genetic diversity or genetic similarity could be helpful in long term selection gain in plants (Adams 1967; Coyne 1968 and Zayed et al. 2005). The breeders worldwide have been given a great attention to this crop. Among pea cultivars/lines germplasm were found wide range of variability in yield and its constituting traits. Hence, genetic variability and diversity is of prime interest to the plant breeder as it plays a key role in framing and successful breeding program. The genetically diverse parents are always able to produce high heterotic effects and great frequency of desirable segregants in further generations as already reported by earlier workers (Kumaran et al. 1995 and Singh 1995). By hybridization between different varieties of the important characters we got a lot of different families in the characteristics (color of flower- flowering date plant height- pod length- pod width- no. seeds/pod- no. ovules/pod-weight of 100 green, dry seeds, podshattering, seeds color, seed texture, green pod yield and dry seed yield) which can be selected where all peas are used as green, cooking, freezing, drying, as well as the production of dry seeds that can be soaked in water and used in cooking such as green seeds. (Kellenbarger et al. 1947; Hillman 1955 and Lamprecht 1956). The further identification of flower color, seed color and/or shape linked to quality and desired traits for customer will provide links to pathways and markers for improved selection processes. The loss or retention of green colour by pea seeds is an economically significant quality parameter. Lines with stable green colour have been identified and used to develop recombinant inbred lines with associated maps to define genetic loci involved in seed colour stability. Crossing between Mammoth melting sugar and Master-B has given rise to new types with certain different combinations of characters and a careful study is required to place the resultant types in appropriate groups. The average amylase content in the starch in wrinkled-seed types is higher than round peas, this high percentage of amylose makes the wrinkled-seeded varieties more sweet (Kellenbarger et al. 1951). This information is important for breeding both in cultivar/line population and in cross progenies. Under southern Egypt condition, previous studies of peas breeding were directed mainly to either evaluation of limited number of selected cultivars (El-Murabaa 1965, El-Shobakey 1985, Kandeel 1990, Ali et al. 1994 and Abdou et al. 1999a) or analysis of combining ability and gene action based on crosses from such fixed-set of parents (Shalaby 1974; Waly and Abd El-Aal 1986; El-Murabaa et al. 1988 a and b; Zayed et al. 1998, Abdou et al. 1999b; Zayed 1999; Zayed and Faris 1999; Zayed et al. 2005; El-Dakkak et al. 2009; El-Dakkak et al. 2014 and Baghdady et al. 2015), indicating that Master-B cv. could be used as progenitors for studied traits in genetic improvement by means of selection in the segregating generations and found that maximum true heterosis in

desirable direction (61.5%) was recorded for pods/plant followed by fresh pod yield(60.2%). Therefore, in the present study an attempt has been made to identify genetic divergent lines in advanced generation, so as to select the potential lines for breeding program to attain the anticipated improvement in green pod yield of pea. The problem of shattering pods and seeds fall on the ground, causing substantial economic loss to the farmers, so they do not overload Producing pods considered a major achievement provides a lot of money and increases the production of seed yield and thus increases economic returns for farmers. The objective of the present study, therefore, was to investigate breeding implication and the potential of variability in pea for the best traits through evaluation of the color impact on the performance of the segregation families for cross (Master-B x Mammoth melting sugar) which grown in the winter seasons for classification the genetic variance, and selection many lines for the objective of the various agricultural as Pod color, size, Seed color and shape. Both size and texture are also considered as premium traits as these attributes affect the price of the pods or seeds yield in the market.

## **MATERIALS AND METHODS**

The present study was carried out during the four successive growing winter seasons (2012/13 to 2015/16) at Shandaweel Agricultural Research Station, Research Center, Ministry of Agriculture Egypt. The basic material used in this study consisted of dihybrid cross, Master-B x Mammoth melting sugar ( $F_1$  hybrid), where the two parents of this cross differed in two characteristics i.e. seed shape and seed color. Therefore, all of the  $F_1$  offspring showed only the dominant form (RrYy) for both traits as the following Table: Phenotypes category of seed shape and seed color in  $F_2$  pea population plants.

Genotype (F <sub>1</sub> )	Phenotype (F <sub>1</sub> )	Genotypic ratio (F <sub>1</sub> )	Phenotypic ratio:						
RrYy	Round mottled seed	All alike	All alike						
Seed shape = Round (R) or Wrinkled (r); Seed Color = Mottled (Y) or Green (y). [The dominant (shows up most often) gene or allele is									
represented with a capital le	represented with a capital letter and the recessive gene with a lower case letter of the same letter (e.g. R, r)]								

On October half, 2012 the  $F_1$  was planted to produce  $F_2$  Population which were shown in two population categories *i.e.* mottled seeds and green seeds. The  $F_2$ -population, was raised on 27 October, 2013. The population was represented by 600 plants in which sixty rows of 10 plants, each were planted with plants spaced 20 cm within rows set 60 cm apart. Also, the parents of the population in addition to local check cultivars Entsar-1 and Entsar-2 were grown along side in three rows for each.

The selection intensity was 10% for the studied population. In the winter season of 2014/15, 60 F<sub>3</sub> families of the populations (4 Families as the four previous categories) from the progeny of the selected plants and an equal number of seeds composited from each  $F_2$  plants to give  $F_3$  bulk seeds, in addition to both parents and the check cultivars were grown in three replications in a randomized complete block design with plants spaced 15 cm apart within rows. Observations and selection were made between and within the  $F_3$ population in order to choose the best plants at the differ families (early flowering, high green pod yield and quality in addition to medium 100-seed weight). From the best plants of the previous generation, 10 ones were selected picked each individual and seeds were separately collected to produce the F4 generation (the second cycle of selection) for the family. In winter season of 2015/16, 10-selected F4 families of the population, F<sub>4</sub>-bulk sample, the parents and the check cultivars were evaluated. A randomized complete block design of three replications was applied. Plants were sown in rows 60 cm apart and 15 cm between hills. The sowing date was October 29 for both  $F_3$  and  $F_4$ generations of the two winter seasons of 2014/2015 and 2015/2016. Data were recorded for individual plants on a random sample of ten guarded plants from each family in F<sub>2</sub>, F<sub>3</sub> and F<sub>4</sub> generations for the characters of pod length (cm), number of seeds/pod, number of pods/plant, weight of 100-seeds (g), plant height (cm) and green pod yield (g/plant. The means of the ten plants were subjected to the statistical (Gomez and Gomez. 1984) and genetic analyses the genetic parameters were estimated in F<sub>2</sub>, F<sub>3</sub> and F<sub>4</sub> generations. Expected response = i Hb  $\sigma$  p where  $\sigma$  p = is the phenotypic standard deviation, Hb = broad sense heritability and i = selection intensity. Heritability in broad sense "Hb" =  $\sigma 2$  g /  $\sigma 2$  p. Realized response to selection was expressed as percent change in the population mean relative to both parents, mid-parents and check cv. (Falconer 1981). The Phenotypic (P.C.V.) and genotypic (G.C.V.) Coefficient of variations were estimated according to Burton (1952).

## **RESULTS AND DISCUSSION**

In the base population  $(F_2)$ , the range of the traits values (Table 1) of the green seeds segregates group were 42-57cm (Plant height), 2- 3 (No. of branches), 6.5- 9.9 cm (Pod length), 1.1-1.2 cm (Pod width), 3.1-6.3 g (Pod weight), 16- 28 (No. of pods/ plant), 5- 8 (No. of seeds/ pod), 7-1 0 (No. of ovules/ pod), 41.5 -51.7% (Shelling), 33.4 - 45.9 g (100-fresh seed weight) and 60.8-187.2 g/plant (Fresh pod yield). However, the range in the mottled seed segregates group (the same Table) were 49 - 74 cm (Plant height),1- 3 (No. of branches), 7.3- 11.2 cm (Pod length), 1.1-1.6 cm (Pod width), 3.1- 6.9 g (Pod weight), 11- 25(No. of pods/ plant), 4-8 (No. of seeds/ pod), 7-10(No. of ovules/ pod), 38.5- 52.8% (Shelling), 33.3- 48.7 g (100-fresh seed weight) and 47.6-113.4 g/plant (Fresh pod yield). Most F<sub>2</sub> progenies show strong evidence of transgressive segregation above the parental values of both green and mottled seed segregations for No. of pods/plant, No. of seeds/pod and No. of ovules/pod,

Shelling%, 100- fresh seed weight and Fresh pod yield plant as well as pod length of mottled seeds segregations only. Desirable heterosis of  $F_1$  values above the better parent is evident for plant height, No. of pods/ plant, shelling% and fresh pod yield plant. The  $F_2$  mean in each of No. of pods/ plant (green seed group), No. of ovules/ pod (green seed group), Shelling% (both green and mottled seed groups) and 100- fresh seed weight (mottled seed group) was higher than the comparatively smaller parent mean and  $F_1$  mean. These observations showed that the negative or smaller positive effects of heterosis in  $F_1$  did not continue in  $F_2$ . However, some  $F_2$  plants were distributed beyond the lower limit of smaller parent. This distribution may be caused by transgressive gene interaction in both parents. These results are in agreement with those obtained by Zayed *et al.* (2005), El-Dakkak and Hussien (2009) and El-Dakkak *et al.* (2009).

Table 1. Parental and F<sub>1</sub> mean as well as the range of F<sub>2</sub> progenies.

	Items			Means	5		
	Parent 1	Parent 2	Б	$F_2 G$	reen seed	$F_2 M$	ottled seed
Traits Traits	Farent I	Parent 2	$\mathbf{F}_1$	Mean	Range	Mean	Range
Plant height (cm)	50.00	85.33	65.00	49.86	42- 57	64.08	49- 74
No. of branches	1.67	3.21	2.67	2.33	2-3	2.16	1-3
Pod length (cm)	10.52	10.07	9.70	8.82	6.5-9.9	9.52	7.3-11.2
Pod width (cm)	1.37	1.77	1.53	1.19	1.1-1.2	1.47	1.1-1.6
Pod weight (g)	6.83	7.93	6.38	4.48	3.1-6.3	5.17	3.1-6.9
No. of pods/ plant	9.00	14.67	22.00	21.67	16-28	16.75	11-25
No. of seeds/ pod	7.67	7.00	7.0	6.38	5-8	5.95	4-8
No. of ovules/ pod	9.50	8.67	9.0	8.86	7-10	8.63	7-10
Shelling%	45.10	41.60	45.60	45.31	41.5-51.7	44.91	38.5-52.8
100-fresh seed weight (g)	36.00	43.87	42.10	39.10	33.4-45.9	41.94	33.3-48.7
Fresh pod yield (g/plant)	58.86	108.6	141.0	98.13	60.8-87.2	83.98	47.6-113.4

#### The genetic parameters:

Estimates of the genetic parameters from the generation means (Table 2) indicated significant both additive [d] and dominance [h] gene effects in some traits of the base population, i.e. plant height, No. of pods/ plant, Shelling %, 100-fresh seed weight and Fresh pod yield/plant. F2 mean value of Fresh pod yield/ plant (green seeds group) was found to lie between the mid-parent and high parent values suggesting that the non-additive genetic variances were predominating for this trait and played the major part in the inheritance than other types of gene actions. The potence ratio, which measures the average degree of dominance over all loci was found to be less than unity for plant height, No of branch/plant, Pod width and No. of ovules/ pod. This revealing that, such traits were controlled by partial dominance. However, complete dominance was found in the inheritance of No. of seeds/ pod and 100- fresh seed weight. On the other hand, the potence ratio displayed over dominance in the inheritance of Pod length, Pod weight, No. of pods/ plant, Shelling%, and Fresh pod yield plant, These results are in agreement with those obtained by Zayed (1999); Abdou et al. (1999b); Zayed et al. (2005); El-Dakkak and Hussien (2009). Inbreeding depression was remarkably manifested in the F<sub>2</sub> plants which ranged from 0.64 to 30.39% in green seeds segregations and from 1.51to 40.43% in mottled seed segregations (Table 2). However, Inbreeding depression in green seeds segregations was uniformly less in magnitude than that obtained in the mottled seeds segregations. Broad sense heritability estimates were generally high for all studied traits except for No. of pods/ plant, No. of seeds/ pod and No. of ovules/ pod which have moderate values. High estimates of broad-sense heritability of some traits, i.e. in pod length, pod weight, shelling%, 100- fresh seed weight and fresh pod yield/plant could be due to the large effects of non-additive as measured by over dominance. From the above-mentioned results, therefore, it is demonstrated that a considerable amount of readily fixable variation is present and available for the plant breeder to manipulate. These results are in agreement with those obtained by Zayed et al. (2005) and El-Dakkak and Hussien (2009).

Table 2. The genetic parameters of some pea traits for F <sub>1</sub> population.
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Items	Traits	Plant height	No. of branches	Pod length	Pod width	Pod weight
[m]		67.67**	2.44**	10.29**	1.57**	7.38**
[d]		17.67**	0.77	0.23	0.20	0.55
[h]		-2.67**	0.13	-0.59	-0.03	-1.00*
F <sub>2</sub> Inbreeding depression	Green seeds	-12.50	-12.50	-9.08	-22.67	-13.22
(ID)	Mottled seeds	-19.05	-19.05	-1.85	-10.97	-18.96
Broad sense heritability%		83.43	72.75	76.34	76.92	65.15
Heterosis%	Mid parent	0.00	0.00	-5.75	-2.13	-13.52
Heterosis%	Best parent	-16.82	-27.27	-7.77	-13.21	-19.54
Potence ratio (h/d)	_	0.15	0.17	2.57	0.15	1.82

#### Table 2. Cont.

Items	Tra	its No. of pods/ plant	No. of seeds/ pod	No. of ovules/ pod	Shelling %	100- fresh seed weight	Fresh pod yield plant
		11.83**	7.33**	<u> </u>	43.35**	<u>39.43**</u>	83.56**
[m]							
[d]		2.83**	0.33	0.42	1.75**	3.43**	24.70**
[h]		10.17**	-0.33	-0.08	2.25**	3.53**	57.41**
$F_2$ Inbreeding	Green seeds	-1.52	-8.84	-1.59	-0.64	-9.01	-30.39
depression(ID)	Mottled seeds	-23.88	-14.97	-4.06	-1.51	-2.38	-40.43
Broad sense heritab	ility%	58.68	44.33	55.60	61.24	68.96	68.34
Hatamaria0/	Mid parent	85.92	-4.55	-0.92	5.19	5.43	81.52
Heterosis%	Best parent	50.00	-8.70	-5.26	1.11	-4.03	46.42
Potence ratio (h/d)	1	3.59	1.00	0.19	1.29	1.03	2.32

The results of  $F_3$  generation indicated significant or highly significant differences among genotypes (selected families, parent and bulk population) in the all populations. Means of the selected families, parents and bulk samples, in addition to heritability in broad sense, genotypic (GCV) and phenotypic (PCV) coefficients of Table 3. The range and average of families for stud variability for all studied traits are presented in Tables 3, 4 and 5. Means of 100-seeds weight, No. of pods/ plant and fresh pods yield (Table 3) were higher in round seed compared with wrinkled one of both green and mottled seed while No. of seeds/pod exhibited the reverse trend in both  $F_3$  and  $F_4$  generations.

Table 3. The range and average of families for studied traits in the 4 studied categories of  $F_3$  and  $F_4$  peagenerations.

	Item		Pod length	No. of seeds/pod	100-seeds weight	Plant height	No. of pods/ plant	Fresh pods yield
	WG	Range	8.3-9.6	5-9	14.2-17.3	41-59	15-42	57.6-151.2
	wG	Average	8.77	7.34	15.65	51.83	22.8	90.29
	ЪC	Range	8-9.9	6-9	15.6-21.1	73-151	15-33	68.9-174.4
F <sub>3</sub>	RG	Average	8.86	7.13	18.33	101.0	25.6	127.2
	DM	Range	8.7-9.8	6-9	19.2-21.4	49-72	13-28	89.1-172.3
	RM	Average	9.27	7.83	20.43	54.6	21.1	134.7
	WM	Range	8-11.4	6-10	12.1-24.4	49-70	11-25	53.5-114.7
	VV IVI	Average	9.45	8.33	18.33	58.87	16.45	79.3
D1		Range	8.8-10.2	7.0-8.5	16.9-20.5	44- 53	8-14	43-67
P1		Average	9.2	7.3	19.3	43	12	48
00		Range	8.8-11.3	5-8	18-24.1	66-85	24-32	93-138
P2		Average	9.9	5.7	23.4	73	28	127.6
Entra 1		Range	10.3-10.8	7.1-8.5	21-23.5	39-45	6-10	53-73
Entsar1		Average	10.6	7.3	22.5	41	7	62.9
Entra 2		Range	9.6-10.3	7-9	14.5-16.4	55-65	16-22	82-116
Entsar2		Average	9.9	7.5	15.2	58	20	84.8

WG, RG, RM and WM: wrinkled green seed, Round green seed, Round mottled and wrinkled mottled seed, respectively.

Table 3 cont.

	Item		Pod length	No. of seeds/pod	100-seeds weight	Plant height	No. of pods/ plant	Fresh pods yield
	WG	Range	8.1-9.3	6-9	13.8-17.2	61-142	10-49	53.2-186.0
	WG	Average	8.69	7.71	15.93	89.9	22.6	103.1
	RG	Range	8.9-10.4	6-8	19-24	41-77	21-46	89.9-267.5
$F_4$	KU	Average	9.88	7.71	21.04	58.5	26.63	137.0
	RM	Range	7.7-12.6	5-9	20.2-26.4	61-130	11-47	70.8-256.2
	KM	Average	9.85	7.92	21.45	92.43	25.0	148.0
	WM	Range	7.7-9.8	6-10	13-17	46-151	14-35	71.5-162.8
	VV IVI	Average	9.13	8.21	15.24	84.9	22.4	114.1
D1		Range	9.6-10.5	7-8.5	16.6-19.1	36-48	8-12	48-68
P1		Average	10.1	8	17.5	40	9	53.0
D2		Range	9.2-11.3	5-8	19.3-23.5	68-91	17-28	95-127
P2		Average	9.6	6	22.4	80	24	115.3
Entron1		Range	10.2-10.9	6-9	22.3-25.4	36-45	7-9	57-69
Entsar1		Average	10.7	7	24.1	40	8	61.4
E		Range	9.4-10.3	6-9	14-16.8	60-72	16-22	69-95
Entsar2		Average	9.8	8	15.0	63	21	87.6
WG DG DM	1 110 6		1.0.1	1.5				-

WG, RG, RM and WM: wrinkled green seed, Round green seed, Round mottled and wrinkled mottled seed, respectively.

The results indicated that pedigree selection decreased the genetic variability measured as genotypic coefficient of variability of the studied traits of the two cycles of selection in all types of the population (Tables 4 and 5). For example, in wrinkled mottled type, the GCV of pod length decreased from 10.57 % (F3) to 6.49% (F4) , from 17.43% to 7.45% for 100-seed weight and from 21.70 % to 21.23% for fresh pod yield/plant. These results were expected because

pedigree selection was exerted and direct to one trait (selection criterion). O'Brien *et al.* (1978); Hamed (2012) and El-Dakkak *et al.* (2014). indicated that the genetic coefficient of variability greatly decreased from the first to the second cycle either for single or multiple trait selection. However, the pedigree procedure was the best one in preserving genetic variability after two cycles of selection.

Pod length Phenotypic variance0.2700.2933.271.620.180.660.190.44Genotypic variance0.1590.1772.050.9980.130.470.130.33P.C.V. %5.925.4718.3513.464.829.104.667.77G.C.V. %4.544.2714.5210.574.127.753.926.44Heritability%58.8460.7162.6761.6773.1972.4670.5071.0Realized response to selection (%) relative to:-4.677.417.072.72-13.96-12.28-8.22-9.6Parent-1-4.677.417.072.72-13.96-12.28-8.22-9.6Parent-2-11.41-0.18-0.51-4.55-9.48-7.71-3.44-4.9Mid-parent-8.173.483.14-1.05-11.7810.05-5.89-7.3Bulk population11.4425.5725.1620.084.456.4911.429.7Entsar-1-17.26-6.77-7.08-10.85-18.79-17.2-13.36-14.6Number of seeds/pod-11.41-0.18-0.51-4.55-11.33-9.59-5.41-6.88Number of seeds/pod-11.446.1910.969.047.1410.137.1713.0Phenotypic variance0.7080.1950.740.5670.310.610.321.14P.C.V. % <th></th> <th>, number</th> <th></th> <th></th> <th>o secus ii</th> <th>eight for i</th> <th></th> <th></th> <th>ciono.</th>		, number			o secus ii	eight for i			ciono.
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Items	WG			WM	WG			WM
$\begin{array}{cccccccccccccccccccccccccccccccccccc$									
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Phenotypic variance		0.293						0.49
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Genotypic variance								0.35
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	P.C.V. %				13.46	4.82			7.70
Realized response to selection (%) relative to: Parent-1Parent-2-4.677.417.072.72-13.96-12.28-8.22-9.6Parent-2-11.41-0.18-0.51-4.55-9.48-7.71-3.44-4.9Mid-parent-8.173.483.14-1.05-11.7810.05-5.89-7.3Bulk population11.4425.5725.1620.084.456.4911.429.7Entsar-1-17.26-6.77-7.08-10.85-18.79-17.2-13.36-14.4Entsar-2-11.41-0.18-0.51-4.55-11.33-9.59-5.41-6.8Number of seeds/pod6.8Phenotypic variance0.7080.1950.740.5670.310.610.321.14P.C.V. %16.549.3015.6713.359.8714.239.5216.66G.C.V. %11.466.1910.969.047.1410.137.1713.06Realized response to selection (%) relative to:Parent-228.7725.1437.4246.1428.4728.5032.0036.8Mid-parent12.929.7420.5028.1510.1110.1413.1417.2Bulk population7.474.4414.6921.965.165.188.0512.00Bulk population7.47 <td>G.C.V. %</td> <td></td> <td></td> <td></td> <td>10.57</td> <td>4.12</td> <td>7.75</td> <td>3.92</td> <td>6.49</td>	G.C.V. %				10.57	4.12	7.75	3.92	6.49
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Heritability%	58.84	60.71	62.67	61.67	73.19	72.46	70.50	71.03
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Realized response to selection (%) relative to:								
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Parent-1	-4.67			2.72	-13.96	-12.28		-9.60
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Parent-2	-11.41	-0.18		-4.55	-9.48	-7.71	-3.44	-4.90
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Mid-parent	-8.17	3.48	3.14	-1.05	-11.78	10.05	-5.89	-7.31
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	Bulk population	11.44	25.57	25.16	20.08	4.45	6.49	11.42	9.74
Number of seeds/podPhenotypic variance1.480.4401.511.2370.581.200.571.88Genotypic variance0.7080.1950.740.5670.310.610.321.16P.C.V. %16.549.3015.6713.359.8714.239.5216.66G.C.V. %11.466.1910.969.047.1410.137.1713.0Heritability%47.9944.2948.9945.8252.3350.6556.7461.6Realized response to selection (%) relative to:28.7725.1437.4246.1428.4728.5032.0036.8Mid-parent12.929.7420.5028.1510.1110.1413.1417.2Bulk population7.474.4414.6921.965.165.188.0512.00Cost7.297.3014.1110.1110.1413.1417.2		-17.26	-6.77	-7.08	-10.85	-18.79	-17.2	-13.36	-14.67
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	Entsar-2	-11.41	-0.18	-0.51	-4.55	-11.33	-9.59	-5.41	-6.84
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Number of seeds/pod								
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	Phenotypic variance	1.48	0.440	1.51	1.237	0.58	1.20	0.57	1.88
$\begin{array}{cccccccccccccccccccccccccccccccccccc$		0.708	0.195	0.74	0.567	0.31	0.61	0.32	1.16
Heritability%         47.99         44.29         48.99         45.82         52.33         50.65         56.74         61.6           Realized response to selection (%) relative to:		16.54	9.30	15.67	13.35	9.87	14.23	9.52	16.68
Heritability%         47.99         44.29         48.99         45.82         52.33         50.65         56.74         61.6           Realized response to selection (%) relative to:									13.09
Realized response to selection (%) relative to:           Parent-1         0.55         -2.29         7.30         14.11         -3.65         -3.63         -1.00         2.6           Parent-2         28.77         25.14         37.42         46.14         28.47         28.50         32.00         36.8           Mid-parent         12.92         9.74         20.50         28.15         10.11         10.14         13.14         17.2           Bulk population         7.47         4.44         14.69         21.96         5.16         5.18         8.05         12.0           Entsar-1         0.55         -2.29         7.30         14.11         10.11         10.14         13.14         17.2						52.33			61.60
Parent-1         0.55         -2.29         7.30         14.11         -3.65         -3.63         -1.00         2.60           Parent-2         28.77         25.14         37.42         46.14         28.47         28.50         32.00         36.88           Mid-parent         12.92         9.74         20.50         28.15         10.11         10.14         13.14         17.2           Bulk population         7.47         4.44         14.69         21.96         5.16         5.18         8.05         12.00           Entsar-1         0.55         -2.29         7.30         14.11         10.11         10.14         13.14         17.2	Realized response to selection (%) relative to:								
Parent-2         28.77         25.14         37.42         46.14         28.47         28.50         32.00         36.8           Mid-parent         12.92         9.74         20.50         28.15         10.11         10.14         13.14         17.2           Bulk population         7.47         4.44         14.69         21.96         5.16         5.18         8.05         12.0           Entsar-1         0.55         -2.29         7.30         14.11         10.11         10.14         13.14         17.2		0.55	-2.29	7.30	14.11	-3.65	-3.63	-1.00	2.63
Bulk population7.474.4414.6921.965.165.188.0512.0Entsar-10.55-2.297.3014.1110.1110.1413.1417.2	Parent-2		25.14	37.42	46.14	28.47		32.00	36.83
Bulk population7.474.4414.6921.965.165.188.0512.0Entsar-10.55-2.297.3014.1110.1110.1413.1417.2	Mid-parent	12.92	9.74	20.50	28.15	10.11	10.14	13.14	17.29
Entsar-1 0.55 -2.29 7.30 14.11 10.11 10.14 13.14 17.2			4.44						12.01
									17.29
Entsar-2 -2.13 -4.89 4.44 11.07 -3.65 -3.63 -1.00 2.6	Entsar-2	-2.13	-4.89	4.44	11.07	-3.65	-3.63	-1.00	2.63
100-seeds weight									
		2.16	3.65	9.69	18.53	0.956	5.131	0.633	1.782
								0.450	1.290
									8.76
									7.45
									72.40
Realized response to selection (%) relative to:									
		-18.91	9.02	11.14	-5.03	-8.97	4.74	16.74	-12.91
									-31.96
									-23.61
									5.61
									-36.76
									1.60

Table 4. The genetic parameters and the realized response to selection relative to parent, mid-parents, checks	i.
and bulk of pod length, number of seeds/pod and 100-seeds weight for $F_3$ and $F_4$ pea generations.	

WG, RG, RM and WM: wrinkled green seed, Round green seed, Round mottled and wrinkled mottled seed, respectively.

 Table 5. The genetic parameters and the realized response to selection relative to parents, mid-parent, checks and bulk of plant height, number of pods/plant and fresh pods yield (g/plant) for F<sub>3</sub> and F<sub>4</sub> pea generations.

 T4		F	3			1	4	
Items	WG	RG	RM	WM	WG	RG	RM	WM
Plant height								
Phenotypic variance	137.2	186.0	662.2	67.98	934.8	695.0	99.07	1826.8
Genotypic variance	83.37	118.0	420.1	42.76	660.3	484.7	73.45	1376.0
P.C.V. %	22.60	23.31	27.54	14.01	34.02	26.11	18.24	50.35
G.C.V. %	17.62	18.57	22.18	11.11	28.59	21.81	15.70	43.70
Heritability%	60.76	63.43	63.44	62.90	70.64	69.75	74.14	75.32
Realized response to selection (%) relative to:								
Parent-1	20.53	36.05	114.95	36.91	127.7	152.4	36.45	112.2
Parent-2	-29.00	-19.86	26.62	-19.36	12.35	26.2	-31.78	6.10
Mid-parent	-10.64	0.86	59.36	1.50	49.80	68.27	-9.03	41.47
Bulk population	4.41	17.85	86.20	18.59	7.36	20.59	-34.81	1.39
Entsar-1	26.41	42.68	125.44	43.59	124.7	152.4	36.45	112.20
Entsar-2	-12.15	-0.85	56.66	-0.22	42.67	60.25	-13.37	34.73
Number of pods/plant								
Phenotypic variance	64.11	80.29	160.5	19.89	152.6	55.68	40.59	49.52
Genotypic variance	35.51	47.17	94.6	11.10	113.2	39.87	29.36	34.74
P.C.V. %	35.12	33.65	50.67	27.11	54.71	29.17	30.23	31.44
G.C.V. %	26.14	25.79	38.91	20.25	47.13	24.68	25.70	26.34
Heritability%	55.38	58.74	58.96	55.81	74.18	71.60	72.32	70.15
Realized response to selection (%) relative to:								
Parent-1	90.00	121.92	108.33	37.08	150.9	184.22	134.2	148.67
Parent-2	-18.57	-4.89	-10.71	-41.25	-5.92	6.58	-12.17	-6.75
Mid-parent	14.00	33.15	25.00	-17.75	36.85	55.03	27.76	35.64
Bulk population	14.40	33.62	25.44	-17.46	11.51	26.32	4.10	10.52
Entsar-1	225.71	280.43	257.14	135.0	182.25	219.8	163.5	179.75
Entsar-2	42.50	66.44	56.25	2.81	25.44	42.11	17.11	24.33
Fresh pods yield/plant								
Phenotypic variance	532.99	3683.4	4381.0	484.7	3512.3	1369.2	1270.0	795.6
Genotypic variance	300.90	2316.6	2824.3	295.7	2320.9	1003.5	902.97	586.3
P.C.V. %	25.57	43.30	44.82	27.78	57.50	29.09	26.46	24.73
G.C.V. %	19.21	35.14	35.99	21.70	46.74	24.90	22.31	21.23
Heritability%	56.46	62.89	64.47	61.01	66.08	73.29	71.10	73.69
Realized response to selection (%) relative to:								
Parent-1	88.10	180.4	207.7	65.13	94.47	140.0	154.2	115.2
Parent-2	-29.24	7.36	15.74	-37.88	-10.61	10.32	16.83	-1.09
Mid-parent	2.84	56.03	68.20	-9.73	22.48	51.16	60.07	35.52
Bulk population	6.85	62.12	74.77	-6.20	7.70	32.92	40.75	19.16
Entsar-1	43.55	117.79	134.79	26.01	67.87	107.2	119.38	85.73
Entsar-2	31.24	99.11	114.65	15.20	38.16	70.51	80.56	52.87

WG, RG, RM and WM: wrinkled green seed, Round green seed, Round mottled and wrinkled mottled seed, respectively.

Data of Table 5 showed that the fresh pod yield trait had high GCV/PCV percentage amounted as 81.29% (F<sub>4</sub> WG), 85.60% (F<sub>4</sub> RG), 84.32% (F<sub>4</sub> RM) and 85.85 % (F<sub>4</sub> WM) indicating that about 81% of the phenotypic variances was due to genetic ones. Therefore, this trait might be more genotypically predominant and it would be possible to achieve further improvement in them. However, heritability was ranged from 66.08 %, to 73.69 % for all cases and in line with the data of PCV and GCV for all categories of the population segregations. On the other hand, the estimates of broad sense heritability after the end cycle of selection (Tables 4 and 5) were medium for number seeds/pod in the wrinkled (52.33%), Round of (50.65%) of green seed and only Round of mottled seed (56.74%), while it was of high magnitude for each of all other traits in all categories. These results are in agreement with those obtained by Hussein et al. (2003), Farag et al. (2005) and El-Dakkak et al. (2014)

## **Correlated response to selection:**

Two cycles of pedigree selection for all studied traits are presented in Tables 4 and 5. The realized gain for plant height reached 7.36, 20.59, -34.81 and 1.39% from the bulk sample compared to 124.7, 152.4, 36.45 and 112.20 % from the check cv (Entsar1) in wrinkled green seed, Round green seed, Round mottled and wrinkled mottled seed categories, respectively. However, it could be noticed that selection for this trait in mottled seed (Round and wrinkled) category, generally, was better than any other categories over all comparisons after the 2<sup>nd</sup> cycle. Also, the realized gain for pods yield/plant reached (7.70, 32.92, 40.75 and 19.16%) from the bulk sample compared to (94.47, 140.0, 154.2 and 115.2%) from the female parent (parent 1) in wrinkled green seed, Round green seed, it accompanied by correlated response to increases obtained for this trait by 67.87, 107.2, 119.38 and 85.73 over check cv (Entsar1) in wrinkled green seed, round green seed, round mottled and wrinkled mottled seed categories, respectively. However, it could be noticed that selection for this trait in Round category, generally, was better than any other categories over all comparisons after the  $2^{nd}$  cycle. These results are in line with Hamed (2012), Kumar et al. (2013), El-Dakkak et al. (2014), Baghdady (2015) and Zayed et al. (2015).

It could be concluded from the results, means of 100-seeds weight, No. of pods/ plant and Fresh pods yield were higher in round seed compared with wrinkled one of both green and mottled seed while No. of seeds/pod exhibited the reverse trend in both  $F_3$  and  $F_4$  generations. Selection for pod green yield in round seed category, generally, was better than any other categories over all comparisons after the 2nd cycle.

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# وراثة لون البذور وبعض الصفات الاقتصادية في البسلة أبوبكر عبد العظيم عبده الدقاق

## قسم بحوث الخضر ذاتية التلقيح- معهد بحوث البساتين- مركز البحوث الزراعية

أجريت هذه الدراسة بمحطة البحوث الزراعية - شندويل- محافظة سوهاج خلال الموسم الشتوي للأعوام ٢٠١٣/٢٠١٢ حتى ٢٠١٦/٢٠١٥ .. حيث استخدم هجين الجيل الأول بين صنغين من البسلة (ماستر وماموث ملتنج شوجر) مختلفين في جميع الصفات وخاصة صفات لون البذور وجودة القرون بهدفُ الحصول على العديد من العائلات المختلفةُ وراثياً والتي يمكن الإنتخاب من خلالها لتلبية إحتياجات المنتج والمستهلك . زرعت بذور هجين الجيل الأول في قطاعات كاملة العشوائية ذات ثلاث مكررات وتم تسجيل بيانات على الصفات الإقتصادية , ثم تم الحصول على نباتات الجيل الثاني والتي تم تسجيل البيانات بها على النباتات الفردية على أساس تقسيم لون البذور الخضراء والبذور المبرقشة ، وتم زراعة بذور الجيل الثاني والثالث للحصول على نباتات الجيل الثالث والرابع في تجربة قطاعات كاملة العشوائية ذات ثلاث مكررات وتم تسجيل بيانات على الصفات الإقتصادية في أربعة مجموعات (بذور خضراء مجعدة – بذور خضراء ملساء– بذور مبرقشة ملساء – بذور مبرقشة مجعدة)، ويمكن تلخيص أهم النتائج ذات الأهمية كالتالي: وجود إختلاف معنوى بين التراكيب الوراثية لكل الصفات المدروسة وتفوق الجيل الأول في صفات ( عدد القرون/نبات، نسبة التصافي، محصول القرون الخضراء للنبات)، بينما حدث إنخفاض في قيم متوسطات الجيل الثاني نتيجة التربية الداخلية. درجة التوريث كانت عالية في معظم الصفات في الجيل الاول F1 وكانت الأعلى في طول النبات (٨٣.٤٣ %)، بينما كانت الأقل لصفة عدد البذور/قرن (٤٤.٣٣ %).قوة الهجين كانت ظاهرة بقوة بصفتي عدد قرون النبات (٠.٠%) ومحصول القرون الخضراء للنبات٤٦.٤٢% . أظهرت النتائج معنوية التأثير المضيف والسيادة في صفات( طول النبات-عدد قرون النبات- التصافي- وزن ١٠٠ بذرة- المحصول الأخضر للنبات) ، كما وجد تأثير للسيادة الجزئية في وراثة بعض الصفات مثل (طول النبات-عدد الفروع- عرض القرن- عدد البويضات), وكانت السيادة التامة في (عدد البذور في القرن ووزن ١٠٠ بذرة خضراء), وكانت السيادة فائقة في ( طول القرن، وزن القرن، عدد قرون النبات, نسبة التصافي ومحصول القرون الخضراء للنبات). أظهرت قيم المتوسطات في الجيل الثالث تفوق المجموعة الثانية ذات البذور الخضراء الملساء (RG) عن باقي المجموعات في صفة عدد القرون، وكذلك تفوق المجموعة الثالثة RM (مبرقشة ملساء) في وزن١٠٠ بذرة طازجة وعدالبذور، بينما تفوقت المجموعة الرابعة WM (مبرقشة مجعدة) في طول القرن وعدد البذور وفي الجيل الرابع ظهر تفوق المجموعة الثانية ذات البذور الخضراء الملساء (RG) في طول القرن وجاءت تالية في المحصول الأخضر ، بينما تفوقت المجموعة الثالثة RM (مبرقشة ملساء) في وزن ١٠٠ بذرة طازجة وطول النبات والمحصول الأخضر والتالية في عدد القرون للنبات، و كانت المجموعة الرابعة WM (مبرقشة مجعدة) متفوقة فقط في عدد البذور في القرن عن باقي المجموعات . كان الفرق بين معامل الاختلاف المظهري والوراثي صغيراً ، وأوضحت النتائج أن درجة التوريث على النطاق الواسع كانت عالية في الأربعة مجموعات لجميع الصفات مما يوضح التأثير الوراثي في عملية الانتخاب لهذه الصفات فيما عدا صفة عدد البذور في القرن التي كانت منخفضة نسبيا مما يوضح تأثرها بالبيئة. بعد دورتين من الإنتخاب حدث تقدم إنتخابي وتفوقت المجموعة الثانية ذات البذور الخضراء الملساء في طول النبات وعدد القرون /نبات، بينما تفوقت المجموعة الثالثة (مبرقشة ملساء) في وزن ١٠٠ بذرة عن الصنف (ماستر وانتصار ٢) وفي محصول القرون الخضراء عن الأبوين وصنفي المقارنة (إنتصار ١،٢)، وُكذَلك تفوقت المجموعة الرابعة WM (مبرقشة مُجعدة) في صفة عدد البذور /قُرن علّى الأبوين وصنفي المقّارنة. عامة يتضح منُ النتائج تفوق مجموعات البذور الملساء (خضراء او مبرقشة) عن البذور المجعدة في عدد القرون على النبات وكذلك محصول القرون الخضراء. جميع القراءات والنتائج الوراثية توحى بامكانية الاستمرار في الانتخاب للوصول إلى العديد من السلالات المرغوبة للمنتج والمستهلك والمتميزة في المحصول والجودة. الدراسة تشير إلى إمكانية إنتاج سلالات بسلة محلية عالية الإنتاجية ذات صفات محصولية وبستانية مر غوبة تقلل من الإستيراد.